

SEQUENCE LISTING

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TSUTSUI, HIDEKAZU
KARASAWA, SATOSHI

<120> FLUORESCENT PROTEIN AND CHROMOPROTEIN

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<141> 2005-12-16

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<151> 2004-06-16

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Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
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Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu
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Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Ser His
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Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu	
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Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile	
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Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Ser His	
165 170 175	
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Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met	
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ccc ccg aat cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc	624
Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly	
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caa agt gca aaa ggc ttt aca gtc aag ctg gaa gca cat gct gtg gct	672
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Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
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Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
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Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
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Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
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Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
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Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile	Leu	
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tca aca gcc ttt caa tat gga aac aca aga tgc ttc aca aag tac	cct gca	240
Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr	Pro Ala	
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Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser	Tyr	
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gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc	tgg	336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala	Ser Trp	
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agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat	cat	384
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile	Tyr His	
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ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca	att	432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr	Ile	
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ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag	gtg cta	480
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val	Leu	
145	150	155
160		
aga ggt gat gtg act cag ttt ctt ctg ctc gaa gga ggt ggt tac	cag	528
Arg Gly Asp Val Thr Gln Phe Leu Leu Glu Gly Gly Tyr Gln		
165	170	175
aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca	atg	576
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala	Met	
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ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt	ggc	624
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu	Gly	
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Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
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Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
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Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
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Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
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Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
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Arg Gly Asp Val Thr His Phe Leu Leu Leu Glu Gly Gly Tyr Gln
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Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190

Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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 35 40 45

atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192
 Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
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130 135 140

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ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta 480
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 Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
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 ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc 624
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
 195 200 205

 caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672
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 Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg
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 Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile
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 Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His
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 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr
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 Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly
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 Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly
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 Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala
 180 185 190

Lys Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Thr Arg Glu
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 Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg
 85 90 95

tct ttt ctc ttt gaa gat ggt gca gtt tgc aca gcc agt gca gat ata	336
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Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala	
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 His Phe Gly Asp His Arg Ile Glu Ile Leu Lys Glu Ala Glu Pro Gly
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 85 90 95
 gag gat gga ggc tat ctt acc att cac cag gac aca agc ata cag gga 336
 Glu Asp Gly Gly Tyr Leu Thr Ile His Gln Asp Thr Ser Ile Gln Gly
 100 105 110

gat agc ttt att ttc aag gtt aaa gtc atc ggt gcc aac ttc cct gcc	384
Asp Ser Phe Ile Phe Lys Val Lys Val Ile Gly Ala Asn Phe Pro Ala	
115 120 125	
aat ggt ccc gtg atg cag aag aaa aca gcc gga tgg gaa cca tgc gta	432
Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val	
130 135 140	
gag atg ctt tat cca cgt gac gga gtc ctg tgt ggg cag tcc ttg atg	480
Glu Met Leu Tyr Pro Arg Asp Gly Val Leu Cys Gly Gln Ser Leu Met	
145 150 155 160	
gcc ctg aaa tgc act gat ggt aac cat ttg acg agc cat ctg cga act	528
Ala Leu Lys Cys Thr Asp Gly Asn His Leu Thr Ser His Leu Arg Thr	
165 170 175	
act tac agg tcc aga aag cca gcc aat gcg gtt aat atg cca aaa ttt	576
Thr Tyr Arg Ser Arg Lys Pro Ala Asn Ala Val Asn Met Pro Lys Phe	
180 185 190	
cat ttt gga gac cat cgc att gag ata cta aag gaa gca gaa cca ggc	624
His Phe Gly Asp His Arg Ile Glu Ile Leu Lys Glu Ala Glu Pro Gly	
195 200 205	
aag ttt tat gaa cag tac gaa tca gca gtg gcc agg tac tgt gaa gct	672
Lys Phe Tyr Glu Gln Tyr Glu Ser Ala Val Ala Arg Tyr Cys Glu Ala	
210 215 220	
gca cca tca aag ctt gga cat cac taa	699
Ala Pro Ser Lys Leu Gly His His	
225 230	
<210> 13	
<211> 224	
<212> PRT	
<213> Lobophytum crassum	
<400> 13	
Met Ser Val Ile Lys Gln Glu Met Lys Ile Lys Leu His Met Glu Gly	
1 5 10 15	
Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Asp Gly Lys Gly Lys	
20 25 30	
Pro Tyr Asp Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala	
35 40 45	
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Asn Ala Phe Gln Tyr Gly	
50 55 60	
Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Phe Lys	
65 70 75 80	
Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Ser Tyr Glu	
85 90 95	

Asp Asn Ala Ile Cys Asn Val Arg Ser Glu Ile Ser Met Glu Gly Asp
 100 105 110
 Cys Phe Ile Tyr Lys Ile Arg Phe Asp Gly Lys Asn Phe Pro Pro Asn
 115 120 125
 Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
 130 135 140
 Met Met Tyr Val Arg Asp Gly Phe Leu Met Gly Asp Val Asn Met Ala
 145 150 155 160
 Leu Leu Leu Glu Gly Gly His His Arg Cys Asp Phe Lys Thr Ser
 165 170 175
 Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Tyr Val Asp
 180 185 190
 His Arg Ile Glu Ile Leu Ser His Asp Arg Asp Tyr Ser Lys Val Lys
 195 200 205
 Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Leu Leu Pro Ser Gln Ala
 210 215 220

<210> 14
 <211> 675
 <212> DNA
 <213> Lobophytum crassum

<220>
 <221> CDS
 <222> (1)..(672)

<400> 14
 atg agt gtg att aaa caa gaa atg aag atc aag ctg cat atg gaa gga 48
 Met Ser Val Ile Lys Gln Glu Met Lys Ile Lys Leu His Met Glu Gly
 1 5 10 15
 aat gta aac ggt cat gca ttt gtg att gaa gga gat gga aaa gga aag 96
 Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Asp Gly Lys Gly Lys
 20 25 30
 cct tac gat ggg aca cag act tta aac ctg aca gtg aaa gaa ggc gca 144
 Pro Tyr Asp Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala
 35 40 45
 cct ctc cct ttt tct tac gac atc ttg aca aat gcg ttc cag tac gga 192
 Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Asn Ala Phe Gln Tyr Gly
 50 55 60
 aat aga gca ttc act aaa tat cca gcc gat ata cca gac tat ttc aag 240
 Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Phe Lys
 65 70 75 80
 cag acg ttt ccc gag ggg tat tca tgg gaa aga acc atg agt tat gaa 288
 Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Ser Tyr Glu
 85 90 95

gac aac gcc att tgc aac gtg aga agc gag atc agc atg gaa ggc gac	336
Asp Asn Ala Ile Cys Asn Val Arg Ser Glu Ile Ser Met Glu Gly Asp	
100	105
110	
tgc ttt atc tat aaa att cggtt gat ggc aag aac ttccc ccc aat	384
Cys Phe Ile Tyr Lys Ile Arg Phe Asp Gly Lys Asn Phe Pro Pro Asn	
115	120
125	
ggt cca gtt atg cag aag aaa act ttg aag tgg gaa cca tcc act gag	432
Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu	
130	135
140	
atg atg tac gtg cgt gat ggg ttt ctg atg ggt gat gtt aac atg gct	480
Met Met Tyr Val Arg Asp Gly Phe Leu Met Gly Asp Val Asn Met Ala	
145	150
155	160
ctg ttg ctt gaa gga ggt ggc cat cac cga tgt gac ttc aaa act tcc	528
Leu Leu Leu Glu Gly Gly His His Arg Cys Asp Phe Lys Thr Ser	
165	170
175	
tac aaa gcg aaa aag gtt gtg cag ttg cca gat tat cac tat gtg gac	576
Tyr Lys Ala Lys Val Val Gln Leu Pro Asp Tyr His Tyr Val Asp	
180	185
190	
cat cgt atc gag atc ttg agc cat gac agg gat tac agc aaa gtc aag	624
His Arg Ile Glu Ile Leu Ser His Asp Arg Asp Tyr Ser Lys Val Lys	
195	200
205	
ctg tat gag aat gcg gtt gct cgc tat tct ttg ctg cca agt cag gcc	672
Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Leu Leu Pro Ser Gln Ala	
210	215
220	
tag	675

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
gaaggrtgyg tcaayggrrca y

21

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 16
acvggdccat ydgvaagaaa rtt

23

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (24)..(25)
<223> inosine

<220>
<221> modified_base
<222> (29)..(30)
<223> inosine

<220>
<221> modified_base
<222> (34)..(35)
<223> inosine

<400> 17
ggccacgcgt cgactagtac gggnnnnn gggnnng

36

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18
ccatttcaa agagaaaaga ccttt

25

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
ggccacgcgt cgactagtac

20

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 20
catgagttct taaaatagtc aac

23

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
atggctcttt caaaggcgagg tg

22

<210> 22
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22
gggggatccg accatggctc tttcaaagcg aggtg

35

<210> 23
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
tagaaatgac ctttcatatg acattc

26

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 24
tctgtttcca tattgaaagg ctg

23

<210> 25
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 25
atggtgtctt attcaaagca aggcatcgca ca

32

<210> 26
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 26
cgggatccga ccatggtgtc ttattcaaag caaggcatcg caca

44

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 27
tagaaatgac ctttcatatg acattc

26

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 28
tctgtttcca tattgaaagg ctg

23

<210> 29
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 29
atggtgtctt attcaaagca aggcacatcgca ca 32

<210> 30
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 30
cgggatccga ccatggtgtc ttattcaaag caaggcatcg caca 44

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 31
atggctcttt caaaggcacgg tc 22

<210> 32
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 32
gggggatccg accatggctc tttcaaagca cggtc 35

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<220>
<221> modified_base
<222> (3)
<223> inosine

<220>
<221> modified_base
<222> (9)
<223> inosine

<220>
<221> modified_base
<222> (21)
<223> a, c, g, t, unknown or other

<400> 33
ggnwsbgtna ayggvcayda ntt

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23

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<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<220>
<221> modified_base
<222> (4)
<223> inosine

<220>
<221> modified_base
<222> (15)
<223> inosine

<220>
<221> modified_base
<222> (18)
<223> inosine

<220>
<221> modified_base
<222> (21)
<223> inosine

<400> 34
gtcncttcttgcacnacnngg nccatydgva ggaaa

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35

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 35
ccttgaaaat aaagctatct

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 36
ccctgtatgc ttgtgtcctg

20

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 37
cccgatatccg accatggtgt cttcattggtaaagaa

36

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)
<223> inosine

<400> 38
grragggnwsb gthaayggvc a

21

```

<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

```

```

<400> 39
aactggaaga attcgcgcc gcaggaa

```

27

```

<210> 40
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

```

```

<220>
<221> modified_base
<222> (4)
<223> inosine

```

```

<220>
<221> modified_base
<222> (15)
<223> inosine

```

```

<220>
<221> modified_base
<222> (18)
<223> inosine

```

```

<220>
<221> modified_base
<222> (21)
<223> inosine

```

```

<400> 40
gtcntcttyt gcacnacngg nccatydgva ggaaa

```

35

```

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

```

```

<400> 41
ttgtcaagat atcggaaagcg aacggcagag

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30

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 42
ggccacgcgt cgactagtag

20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 43
cttctcacgt tgcaaatggc

20

<210> 44
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 44
cccgatccg atgagtgtga ttacawcaga aatgaagatg gagc

44